

Page 46, lines 11-19, delete current paragraph and insert therefor:

Repression of a coding sequence of interest may occur within a plant following sequential transformation of a target gene, for example GUS, followed by transformation with an effector gene. To demonstrate the efficacy of this approach, Arabidopsis plants were transformed using standard techniques (Clough and Bent, 1998) using the construct UAS<sub>GAL4</sub>-tCUP-GUS (tCUP-GUS; reporter gene). As shown in Figures 19 (B) and (C), these plants (indicated as control 1, 2) exhibit GUS activity in both leaves and seeds. Transformed plants expressing GUS were then re-transformed with one of two effector constructs, 35S-GAL4/AtHD2A, or NAP1-GAL4/AtHD2A. The levels of GUS activity within the dual transgenics are shown in Figures 19 (B) and (C).

IN THE CLAIMS:

Please cancel claims 10, 20, 21, 23, 25, 27 and 28 without prejudice to or disclaimer of the subject matter contained therein.

Please replace claims 1, 4, 9, 14 and 15 as follows:

4. (Amended) A method of repressing transcription of a coding sequence of interest in a transgenic plant, comprising:

- a) introducing into a plant:
  - i) a first chimeric nucleotide sequence comprising a first regulatory element in operative association with a gene of interest, and a controlling sequence; and
  - ii) a second chimeric nucleotide sequence comprising a second regulatory element in operative association with a nucleotide sequence encoding a histone deacetylase fused with a DNA binding protein, said DNA binding protein interacting with said controlling sequence, to produce said transgenic plant; and

b) growing said transgenic plant.

4. (Amended) The method of claim 1, wherein said histone deacetylase, within said step of introducing, is selected from the group consisting of:

- i) AtRPD3A, AtRPD3B, AtHD2A, or AtHD2B;
- ii) a fragment of AtRPD3A, AtRPD3B, AtHD2A, or AtHD2B; and
- iii) a nucleotide sequence that hybridizes to AtRPD3A, AtRPD3B, AtHD2A, or AtHD2B at 65°C in 0.5 M Na<sub>2</sub>HPO<sub>4</sub> (pH 7.2), 7% SDS, and 1mM EDTA, followed by washing for 15 minutes in 2 x SSC with 0.1% SDS at room temperature, then twice for 20 minutes in 0.1 x SSC, 0.1% SDS at 65°C;

wherein said fragment or nucleotide sequence that hybridizes encodes a product that exhibits repression of gene expression activity.

9. (Amended) An isolated nucleotide sequence, selected from the group consisting of:

- i) SEQ ID NO:3, SEQ ID NO:5, or SEQ ID NO:7;
- ii) a deletion or fragment of SEQ ID NO:3, SEQ ID NO:5, or SEQ ID NO:7; and
- iii) a nucleotide sequence that hybridizes to SEQ ID NO:3, SEQ ID NO:5, or SEQ ID NO:7 at 65°C in 0.5 M Na<sub>2</sub>HPO<sub>4</sub> (pH 7.2), 7% SDS, and 1 mM EDTA, followed by washing for 15 minutes in 2 x SSC with 0.1% SDS at room temperature, then twice for 20 minutes in 0.1 x SSC, 0.1% SDS at 65°C;

wherein said fragment, said deletion, or said nucleotide sequence that hybridizes encodes a product that exhibits repression of gene expression activity.

14. (Amended) A transgenic plant cell produced by the method of claim 1.

15. (Amended) A transgenic plant produced by the method of claim 1.

Please add new claims 29-31 as follows:

--29. The method of claim 1 wherein said histone deacetylase, within said step of introducing, is selected from the group consisting of:

- i) a fragment or deletion of *AtRPD3A*, *AtRPD3B*, *AtHD2A*, or *AtHD2B*;
- ii) a nucleotide sequence that hybridizes to a fragment or deletion of *AtRPD3A*, *AtRPD3B*, *AtHD2A*, or *AtHD2B* at 65EC in 0.5 M Na<sub>2</sub>HPO<sub>4</sub> (pH 7.2), 7% SDS, and 1mM EDTA, followed by washing for 15 minutes in 2 x SSC with 0.1% SDS at room temperature, then twice for 20 minutes in 0.1 x SSC, 0.1% SDS at 65EC; and
- iii) a nucleotide sequence that is at least 80% identical to SEQ ID NO:3, SEQ ID NO:5, or SEQ ID NO:7, or a fragment thereof;

wherein said fragment, said deletion, or said nucleotide sequence that hybridizes to a fragment or deletion, encodes a product that exhibits repression of gene expression activity.--

--30. An isolated nucleotide sequence, selected from the group consisting of:

- i) a nucleotide sequence that is at least 80% identical to SEQ ID NO:3, SEQ ID NO:5, or SEQ ID NO:7, or a fragment thereof, and
- ii) a fragment of SEQ ID NO:3, SEQ ID NO:5, or SEQ ID NO:7;

wherein said fragment or said nucleotide sequence that is at least 80% identical encodes a product that exhibits repression of gene expression activity.--

--31. An isolated nucleotide sequence selected from the group consisting of SEQ ID NO:3, SEQ ID NO:5 and SEQ ID NO:7.--